#1

UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/530,844	04/08/2005	Susanne Leonhartsberger	Leonhartsberger	3625

25889 7590 08/24/2006

WILLIAM COLLARD
COLLARD & ROE, P.C.
1077 NORTHERN BOULEVARD
ROSLYN, NY 11576

EXAMINER	
RAGHU, GANAPATHIRAM	
ART UNIT	**PAPER NUMBER**
1652	

DATE MAILED: 08/24/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/530,844	LEONHARTSBERGER ET AL.	
	Examiner	Art Unit	
	Ganapathirama Raghu	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE ____ MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *07 July 2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-9* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-9* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *05/09/05*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *SEQ ALIGN*.

DETAILED ACTION

Claims 1-9 are pending in this application are now under consideration for examination.

Election/Restrictions

Applicant's election with traverse of Group II, claims 1-9 for prosecution in their response dated 07 July 2006 is acknowledged. The applicants' have requested reconsideration of restriction requirement (Groups II, III and IV) as the instant application claims a homoserine transsuccinylase with defined technical features, wherein the carboxy terminus of said enzyme is modified with insertions of defined polypeptides varying in sequence and length, i.e., to SEQ ID NO: 2 following the deletion of carboxy terminus (amino acid residues 297 onwards), the peptides with the SEQ ID NOs: 8 or 10 or 12 have been inserted and that any search of for the species of Group II would necessarily include a search of the species in Groups III and IV. The applicants' arguments are persuasive and therefore restriction is withdrawn and all species in groups II, III and IV are being examined.

Priority

Acknowledgment is made of applicants' claim for foreign priority under 35 U.S.C. 119(a)-(d). This application is a 371 PCT/EP03/11486 filed on 10/16/2003 and claims the priority date of German application 102 49 642.0 filed on 10/24/2002. The examiner notes that no English translation has been filed for the German application and therefore for all examination purposes the 371 PCT/EP03/11486 filing date is considered as the priority date.

Information Disclosure Statement

The information disclosure statement (IDS) submitted on 09 May 2005 is in compliance with the provisions of 37 CFR 1.97. Accordingly, the information disclosure statement is being considered by the examiner.

Drawings

Drawings are accepted for examination purposes only.

Specification

The disclosure is objected to because of the following informalities:

The specification contains drawing, however applicants have not provided any description for the figure. Correction is required.

Claim Objections

Claims 1, 3 and 9 are objected, due to the following informality: The following claims contain abbreviations; Claims 1, 3 and 9 have SAM in their claims. Examiner suggests at least in the first recitation of the abbreviations, expanding them to recite the full forms of what the abbreviation stands for. Appropriate correction is required.

Claim Rejections: 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claim 1 and dependent claims 2-9 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claim 1 recites "...this change..". Claim previously sated that "at least 2 amino acid changes" in line 9. Is "this change" in both the amino acids or change is in only one amino acid? Clarification and correction is required.

Claim 8 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claim 1 recites the phrase "...preferably". Does the claim only includes a specific strain of *E.coli* only or other gram-negative including *E.coli* strains. Clarification is required.

Claim Rejections 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claim 1 and claims 2-3 and 5-9 depending therefrom are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claims 1-3 and 5-9, are directed to a mutant homoserine transsuccinylase with reduced sensitivity to L-methionine or SAM as compared to the wild-type enzyme comprising the

constituent sequence of TyrGlnXaaThrPro with the Thr being between position 285 and 310 and said mutant exhibits a change of at least two amino acids as compared to the wild-type enzyme, said change being in the Thr or C-terminally thereof, a metA allele encoding homoserine transsuccinylase, vector comprising said mutant, transformed host cell and the method of preparing L-methionine or SAM. Claims 1-3 and 5-9 are rejected under this section 35 U.S.C. 112, because the claims are directed to any or all homoserine transsuccinylase comprising the constituent sequence of TyrGlnXaaThrPro at position 285-310, involves a genus of polypeptides including variants, mutants and recombinants form any source with no support in the specification for the structural details associated with the function i.e., homoserine transsuccinylase activity with reduced sensitivity to L-methionine or SAM. No description of identifying characteristics of all of the polypeptides of an isolated homoserine transsuccinylase, including variants, mutants and recombinants from any source has been provided by the applicants in the specification. No information, beyond the characterization of the polypeptide, homoserine transsuccinylase from *E.coli* wild-type enzyme of SEQ ID NO: 2 and three mutants, wherein the amino acid residues 297 onwards of said wild-type enzyme sequence has been replaced with SEQ ID NO: 8 or 10 or 12 said mutants with reduced sensitivity to L-methionine or SAM has been provided by the applicants, which would indicate that they had possession of the claimed genus of all of the polypeptides of an isolated homoserine transsuccinylase with reduced sensitivity to L-methionine or SAM, including variants, mutants and recombinants form any source. Therefore, one skilled in the art cannot reasonably conclude that applicant had possession of the claimed invention at the time the instant application was filed. Applicant is referred to the revised guidelines concerning compliance with the written description

requirement of U.S.C. 112, first paragraph, published in the Official Gazette and also available at www.uspto.gov.

Claims 1-3 and 5-9 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated homoserine transsuccinylase, said wild-type enzyme isolated from *E.coli* and comprising the sequence of SEQ ID NO: 2 and three mutants derived by deleting the amino acid residues 297 onwards in said wild-type enzyme carboxy terminus and replaced with the polypeptide sequence of SEQ ID NO: 8 or 10 or 12 and said mutants exhibit reduced sensitivity to L-methionine or SAM, vector comprising polynucleotides encoding said polypeptides, host cell and method of preparing L-methionine or SAM, does not reasonably provide enablement for any or all homoserine transsuccinylase comprising the constituent sequence of TyrGlnXaaThrPro at position 285-310, including variants, mutants and recombinants with reduced sensitivity to L-methionine or SAM form any source, vector comprising polynucleotides encoding said polypeptides, host cell and method of preparing L-methionine or SAM. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and or use the invention commensurate in scope with the claim.

Factors to be considered in determining whether undue experimentation is required are summarized in *In re Wands* (858 F.2d 731, 8 USPQ 2nd 1400 (Fed. Cir. 1988)) as follows: (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the

prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claim(s).

Claims 1-3 and 5-9 are so broad as to encompass any or all homoserine transsuccinylase comprising the constituent sequence of TyrGlnXaaThrPro at position 285-310, including variants, mutants and recombinants form any source with reduced sensitivity to L-methionine or SAM, vector comprising polynucleotides encoding said polypeptides, host cell and method of preparing L-methionine or SAM. The scope of the claims is not commensurate with the enablement provided by the disclosure with regard to the extremely large number of polypeptides with homoserine transsuccinylase activity broadly encompassed by the claims. Since the amino acid sequence of a protein encoded by a polynucleotide determines its structural and functional properties, predictability of which changes can be tolerated in a protein's amino acid sequence and obtain the desired activity requires knowledge and guidance with regard to which amino acids in the protein's sequence and the respective codons in its polynucleotide, if any, are tolerant of modification and which are conserved (i.e. expectedly intolerant to modification), and detailed knowledge of the ways in which the encoded proteins' structure relates to its function. However, in this case the disclosure is limited to an isolated homoserine transsuccinylase, said wild-type enzyme isolated from *E.coli* and comprising the sequence of SEQ ID NO: 2 and three mutants derived by deleting the amino acid residues 297 onwards in said wild-type enzyme carboxy terminus and replaced with the polypeptide sequence of SEQ ID NO: 8 or 10 or 12 and said mutants exhibit reduced sensitivity to L-methionine or SAM, vector comprising polynucleotides encoding said polypeptides, host cell and method of preparing L-methionine or SAM. In view of the great breadth of the claims, amount of experimentation

required to make the claimed polypeptides the lack of guidance, working examples, and unpredictability of the art in predicting function from a polypeptide primary structure (e.g., see Ngo et al. in The Protein Folding Problem and Tertiary Structure Prediction, 1994, Merz et al. (ed.), Birkhauser, Boston, MA, pp. 433 and 492-495), the claimed invention would require undue experimentation. As such, the specification fails to teach one of ordinary skill how to use the full scope of the polypeptides encompassed by this claim.

While enzyme isolation techniques, recombinant and mutagenesis techniques are known, and it is not routine in the art to screen for multiple substitutions or multiple modifications as encompassed by the instant claims, the specific amino acid positions within a protein's sequence where amino acid modifications can be made with a reasonable expectation of success in obtaining the desired activity/utility are limited in any protein and the result of such modifications is unpredictable. In addition, one skilled in the art would expect any tolerance to modification for a given protein to diminish with each further and additional modification, e.g. multiple substitutions or deletions.

The specification does not support the broad scope of the claims for any or all homoserine transsuccinylase comprising the constituent sequence of TyrGlnXaaThrPro at position 285-310, including variants, mutants and recombinants form any source with reduced sensitivity to L-methionine or SAM, vector comprising polynucleotides encoding said polypeptides, host cell and method of preparing L-methionine or SAM, because the specification does not establish: (A) regions of the protein/polynucleotide structure which may be modified to produce the desired effect on the encoded homoserine transsuccinylase with reduced sensitivity to L-methionine or SAM wherein the polypeptides are from any source; (B) the general tolerance

of the polypeptide and the polynucleotide encoding homoserine transsuccinylase activity to modification and extent of such tolerance; (C) a rational and predictable scheme for modifying any amino acid residue or the respective codon in the polynucleotide with an expectation of obtaining the desired biological function, i. e., homoserine transsuccinylase mutants exhibiting reduced sensitivity to L-methionine or SAM; and (D) the specification provides insufficient guidance as to which of the essentially infinite possible choices is likely to be successful.

Thus, applicants have not provided sufficient guidance to enable one of ordinary skill in the art to make and use the claimed invention in a manner reasonably correlated with the scope of the claims which broadly encompass any or all homoserine transsuccinylase comprising the constituent sequence of TyrGlnXaaThrPro at position 285-310, including variants, mutants and recombinants form any source with reduced sensitivity to L-methionine or SAM, vector comprising polynucleotides encoding said polypeptides, host cell and method of preparing L-methionine or SAM. The scope of the claims must bear a reasonable correlation with the scope of enablement (*In re Fisher*, 166 USPQ 19 24 (CCPA 1970)). Without sufficient guidance, determination of polynucleotides and encoding polypeptides of homoserine transsuccinylase activity having the desired biological characteristics is unpredictable and the experimentation left to those skilled in the art is unnecessarily, and improperly, extensive and undue. See *In re Wands* 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988).

Claim Rejections 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1, 3 and 5-9 are rejected under 35 U.S.C. 102(b) as being anticipated by patent assigned to AJINOMOTO (JP 2000139471 A, published 05/23/2000) when given the broadest interpretation. Claims 1-3 and 5-9 are directed to a mutant homoserine transsuccinylase with reduced sensitivity to L-methionine or SAM as compared to the wild-type enzyme comprising the constituent sequence of TyrGlnXaaThrPro with the Thr being between position 285 and 310 and said mutant exhibits a change of at least two amino acids as compared to the wild-type enzyme, said change being in the Thr or C-terminally thereof, a metA allele encoding homoserine transsuccinylase, vector comprising said mutant, transformed host cell and the method of preparing L-methionine or SAM. Patent assigned to AJINOMOTO (JP 2000139471 A, published 05/23/2000) disclose preparing L-methionine with a modified Met producing microorganism (*E.coli*) deleted for a repressor of the Met biosynthetic system, capable of producing Met, particularly with enhanced homoserine transuccinylase activity and released of concerted inhibition with Met and SAM and a DNA encoding a homoserine transuccinylase having a variation at Ile296 to Ser and Pro298 to Leu of SEQ ID NO: 2 (change in constituent sequence of TyrGlnXaaThrPro or in Thr or C-terminally thereof of wild-type metA allele encoding homoserine transsuccinylase). Therefore the reference of AJINOMOTO (JP 2000139471 A, published 05/23/2000, claiming the priority of 1998JP-0326717 filed on 11/17/1988) anticipates the claims 1, 3 and 5-9 as written.

Claims 1-3 are rejected under 35 U.S.C. 102(b) as being anticipated by Nelson et al., (Nature 1999, Vol. 399: 323-329) when given the broadest interpretation. Claims 1-3 are directed to a mutant homoserine transsuccinylase with reduced sensitivity to L-methionine or SAM as compared to the wild-type enzyme comprising the constituent sequence of TyrGlnXaaThrPro with the Thr being between position 285 and 310 and said mutant exhibits a change of at least two amino acids as compared to the wild-type enzyme, said change being in the Thr or C-terminally thereof, furthermore said change is of at least 5-10 amino acids. Nelson et al., (*supra*) disclose a homoserine transuccinylase from *Thermotoga maritima* having a C-terminal variation from amino acid residues 296 onwards, having carboxy terminus of YQKTPY (amino acid residues 293-298; see sequence alignment provided), the sequence disclosed by Nelson et al., lacks the amino acid residues at the carboxy terminus spanning from 299-309 of the wild-type sequence of SEQ ID NO: 2 of the instant application. Said reference is silent regarding the sensitivity to L-methionine or SAM, however examiner takes the position that said homoserine transsuccinylase has a variation in the carboxy terminus other than the constituent sequence of TyrGlnXaaThrPro and therefore the polypeptide disclosed by Nelson et al., should also possess similar biochemical properties. Therefore the reference of Nelson et al., (*supra*) anticipates the claims 1-3 as written.

Claims 1-3 are rejected under 35 U.S.C. 102(b) as being anticipated by Goodner et al., (Science 2001, Vol. 294: 2323-2328) when given the broadest interpretation. Claims 1-3 are directed to a mutant homoserine transsuccinylase with reduced sensitivity to L-methionine or SAM as compared to the wild-type enzyme comprising the constituent sequence of

TyrGlnXaaThrPro with the Thr being between position 285 and 310 and said mutant exhibits a change of at least two amino acids as compared to the wild-type enzyme, said change being in the Thr or C-terminally thereof, furthermore said change is of at least 5-10 amino acids. Goodner et al., (*supra*) disclose a homoserine transuccinylase from *Agrobacterium tumefaciens* having a C-terminal variation from amino acid residues 296 onwards, having a carboxy terminus of WRSHAHLFFGNWINEIQY (amino acid residues 285-302; see sequence alignment provided), the sequence disclosed by Goodner et al., lacks the amino acid residues at the carboxy terminus spanning from 299-309 of the wild-type sequence of SEQ ID NO: 2 of the instant application. Said reference is silent regarding the sensitivity to L-methionine or SAM, however examiner takes the position that said homoserine transsuccinylase has a variation in the carboxy terminus other than the constituent sequence of TyrGlnXaaThrPro and therefore the polypeptide disclosed by Goodner et al., should also possess similar biochemical properties. Therefore the reference of Goodner et al., (*supra*) anticipates the claims 1-3 as written.

Claims 1-3 are rejected under 35 U.S.C. 102(b) as being anticipated by DelVecchio et al., (PNAS 2002, Vol. 99 (1): 443-448) when given the broadest interpretation. Claims 1-3 are directed to a mutant homoserine transsuccinylase with reduced sensitivity to L-methionine or SAM as compared to the wild-type enzyme comprising the constituent sequence of TyrGlnXaaThrPro with the Thr being between position 285 and 310 and said mutant exhibits a change of at least two amino acids as compared to the wild-type enzyme, said change being in the Thr or C-terminally thereof, furthermore said change is of at least 5-10 amino acids. DelVecchio et al., (*supra*) disclose a homoserine transuccinylase from *Brucella melitensis*

having a C-terminal variation from amino acid residues 296 onwards, having a carboxy terminus of SHAHLFFGNWINEMYQST (amino acid residues 285-312; see sequence alignment provided), the sequence disclosed by DelVecchio et al., lacks the amino acid residues at the carboxy terminus spanning from 299-309 of the wild-type sequence of SEQ ID NO: 2 of the instant application. Said reference is silent regarding the sensitivity to L-methionine or SAM, however examiner takes the position that said homoserine transsuccinylase has a variation in the carboxy terminus other than the constituent sequence of TyrGlnXaaThrPro and therefore the polypeptide disclosed by DelVecchio et al., should also possess similar biochemical properties. Therefore the reference of DelVecchio et al., (*supra*) anticipates the claims 1-3 as written.

Conclusion

None of the claims are allowed.

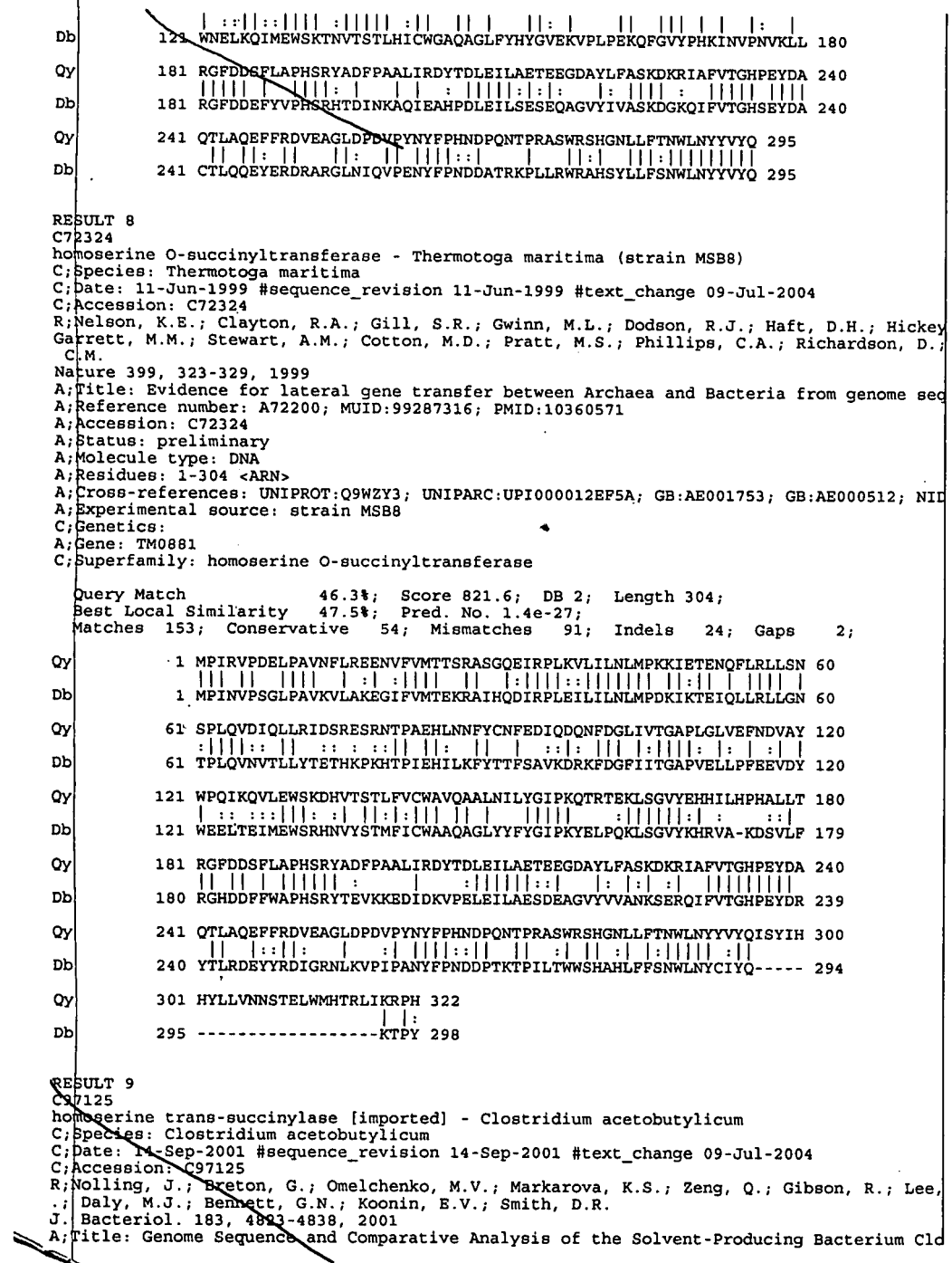
Any inquiry concerning this communication or earlier communications from the examiner should be directed to Ganapathirama Raghu whose telephone number is 571-272-4533. The examiner can normally be reached on 8 am - 5 pm. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapu Achutamurthy can be reached on 571-272-0928. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300 for regular communications and for After Final communications. Any inquiry of a general nature or relating to the status of the application or proceeding should be directed to the receptionist whose telephone number is 571-272-1600.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Ganapathirama Raghu, Ph.D.
Patent Examiner
Art Unit 1652
Aug. 06, 2006.

REBECCA E. PRUITY
PRIMARY EXAMINER
GROUP 1600

```
Qy        181 RGFDDSFLAPHSRYADFPAALIRDYTDLEILAETEEGDAYLFASKDKRIAFVTGHPEYDA 240
              || | |  | ||: :   | |  : :|||| |::|     |   |      ::  | |||:
Db        181 NGFSDDFQVPVSRWTEVRRADIEKHPELEILMESDEMGVCLAHEKAGNRLYMFNHVEYDS 240

Qy        241 QTLAQEFFRDVEAGLDPDVPYNYFPHNDPQNTPRASWRSHGNLLFTNWLNYYVYQ 295
              :|| |:|||| :|:   :|::|||||||:  |   |||| :| | ||:|  :||
Db        241 TSLADEYFRDVNSGVPIKLPHDYFPHNDPELAPLNRWRSHAHLFFGNWIN-EIYQ 294


RESULT 14
C97685
homoserine O-succinyltransferase (homoserine o-transsuccinylase) (hts) [imported] - Agrc
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 07-Jul-2003
C;Accession: C97685
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C97685
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-316 <KUR>
A;Cross-references: UNIPARC:UPI00000D1FCF; GB:AE007869; PIDN:AAK88436.1; PID:g15157931;
C;Genetics:
A;Gene: AGR_C_4927
A;Map position: circular chromosome
C;Superfamily: homoserine O-succinyltransferase

  Query Match          40.1%;  Score 710.9;  DB 2;  Length 316;
  Best Local Similarity  45.4%;  Pred. No. 9.4e-23;
  Matches  134;  Conservative   57;  Mismatches  103;  Indels    1;  Gaps    1;

Qy          1 MPIRVPDELPAVNFLREENVFVMTTSRASGQEIRPLKVLILNLMPKKIETENQFLRLLSN 60
              |||::||  |||    |  | | ||| : |  |:||||:: :||||| ||:|| |  ||:
Db          9 MPIKIPDTLPAFETLVHEGVRVMTETAAIRQDIRPLQIGLLNLMPNKIKTEIQMARLVGA 68

Qy         61 SPLQVDIQLLRIDSRESRNTPAEHLNNFYCNFEDIQDQNFDGLIVTGAPLGLVEFNDVAY 120
              |||||:: |:||    ::||| ||| :||  :|::: : ||| |:||||: |::: || |
Db         69 SPLQVELSLIRIGGHRAKNTPEEHLLSFYQTWEEVRHRKFDGFIITGAPIELLDYEDVTY 128

Qy        121 WPQIKQVLEWSKDHVTSTLFVCWAVQAALNILYGIPKQTRTEKLSGVYEHHILHPHALLT 180
              | ::|: ||:: :| ||| |||   ||:  :|:||    ||  ||| |  | | ::
Db        129 WNEMQQIFEWTQTNVHSTLNVCWGAMAAIYHFHGVPKYELKEKAFGVYRHRNLSPSSIYL 188

Qy        181 RGFDDSFLAPHSRYADFPAALIRDYTDLEILAETEEGDAYLFASKDKRIAFVTGHPEYDA 240
              || | |  | ||: :   | |  : :|||| |::|     |   |      ::  | |||:
Db        189 NGFSDDFQVPVSRWTEVRRADIEKHPELEILMESDEMGVCLAHEKAGNRLYMFNHVEYDS 248

Qy        241 QTLAQEFFRDVEAGLDPDVPYNYFPHNDPQNTPRASWRSHGNLLFTNWLNYYVYQ 295
              :|| |:|||| :|:   :|::|||||||:  |   |||| :| | ||:|  :||
Db        249 TSLADEYFRDVNSGVPIKLPHDYFPHNDPELAPLNRWRSHAHLFFGNWIN-EIYQ 302


RESULT 15
AD3607
homoserine o-succinyltransferase (EC 2.3.1.46) [imported] - Brucella melitensis (strain
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 07-Jul-2003
C;Accession: AD3607
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AD3607
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-322 <KUR>
A;Cross-references: UNIPARC:UPI00000585FA; GB:AE008918; PIDN:AAL54023.1; PID:g17984975;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0781
A;Map position: II
C;Superfamily: homoserine O-succinyltransferase
C;Keywords: acyltransferase; coenzyme A

  Query Match          36.5%;  Score 647.1;  DB 2;  Length 322;
  Best Local Similarity  38.8%;  Pred. No. 5.6e-20;
  Matches  124;  Conservative   61;  Mismatches  106;  Indels   29;  Gaps    3;

Qy          1 MPIRVPDELPAVNFLREENVFVMTTSRASGQEIRPLKVLILNLMPKKIETENQFLRLLSN 60
              |||::||:||| : |  | | +|  : |  |:|||:: :||||| |: || |  |||
Db         17 MPIKIPDDLPATSVLEAEGVMVMREADAVRQDIRPLRIGLLNLMPNKVTTETQIARLLGA 76

Qy         61 SPLQVDIQLLRIDSRESRNTPAEHLNNFYCNFEDIQDQNFDGLIVTGAPLGLVEFNDVAY 120
              :||||:: |:|: :  :|:|||:|: :||| :|:: || ||| ::|||:  : | :| |
Db         77 TPLQVELTLVRMTNHVARHTPADHMLSFYCPWEEVNDQRFDGFVITGAPVERLPFEEVTY 136

Qy        121 WPQIKQVLEWSKDHVTSTLFVCWAVQAALNILYGIPKQTRTEKLSGVYEHHILHPHALLT 180
              | ::::| :|:: ||  || :||| |||:   :|: |     | |||:    |   :
Db        137 WDEMRRVFDWTQSHVHRTLNICWAAQAAVYHFHGMKKYDLPAKASGVFRQRSLVLASPYL 196

Qy        181 RGFDDSFLAPHSRY-----ADFPAALIRDYTDLEILAETEEGDAYLFASKDKRIAFVTGH 235
              ||| | |  | ||:     :| ||      : |::| :: |    |       |   : |
Db        197 RGFSDDFAIPVSRWTEVRKSDIPAD-----SGLKVLVDSTETGLCLLDDPRHRSLHMFNH 251

Qy        236 PEYDAQTLAQEFFRDVEAGLDPDVPYNYFPHNDPQNTPRASWRSHGNLLFTNWLNYYVYQ 295
              |||  :|| |:|||::   :  || |||| :|: :  |   |||| :||| ||:|
Db        252 VEYDTTSLADEYFRDIQVQPEAKVPVNYFPGDDAKRPPENRWRSHAHLLFGNWIN----- 306

Qy        296 ISYIHHYLLVNNSTELWMHT 315
                           |::  |
Db        307 -------------EMYQST 312


Search completed: August  1, 2006, 04:30:16
Job time : 22.8385 secs
```



Db 121 WNELKQIMEWSKTNVTSTLHICWGAQAGLFYHYGVEKVPLPEKQFGVYPHKINVPNVKLL 180

Qy 181 RGFDDSFLAPHSRYADFPAALIRDYTDLEILAETEEGDAYLFASKDKRIAFVTGHPEYDA 240

Db 181 RGFDDEFYVPHSRHTDINKAQIEAHPDLEILSESEQAGVYIVASKDGKQIFVTGHSEYDA 240

Qy 241 QTLAQEFFRDVEAGLDPDVPYNYFPHNDPQNTPRASWRSHGNLLFTNWLNYYVYQ 295

Db 241 CTLQQEYERDRARGLNIQVPENYFPNDDATRKPLLRWRAHSYLLFSNWLNYYVYQ 295

RESULT 8
C72324
homoserine O-succinyltransferase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: C72324
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: C72324
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-304 <ARN>
A;Cross-references: UNIPROT:Q9WZY3; UNIPARC:UPI000012EF5A; GB:AE001753; GB:AE000512; NID
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0881
C;Superfamily: homoserine O-succinyltransferase

Query Match 46.3%; Score 821.6; DB 2; Length 304;
Best Local Similarity 47.5%; Pred. No. 1.4e-27;
Matches 153; Conservative 54; Mismatches 91; Indels 24; Gaps 2;

Qy 1 MPIRVPDELPAVNFLREENVFVMTTSRASGQEIRPLKVLILNLMPKKIETENQFLRLLSN 60

Db 1 MPINVPSGLPAVKVLAKEGIFVMTEKRAIHQDIRPLEILILNLMPDKIKTEIQLLRLLGN 60

Qy 61 SPLQVDIQLLRIDSRESRNTPAEHLNNFYCNFEDIQDQNFDGLIVTGAPLGLVEFNDVAY 120

Db 61 TPLQVNVTLLYTETHKPKHTPIEHILKFYTTFSAVKDRKFDGFIITGAPVELLPFEEVDY 120

Qy 121 WPQIKQVLEWSKDHVTSTLFVCWAVQAALNILYGIPKQTRTEKLSGVYEHHILHPHALLT 180

Db 121 WEELTEIMEWSRHNVYSTMFICWAAQAGLYYFYGIPKYELPQKLSGVYKHRVA-KDSVLF 179

Qy 181 RGFDDSFLAPHSRYADFPAALIRDYTDLEILAETEEGDAYLFASKDKRIAFVTGHPEYDA 240

Db 180 RGHDDFFWAPHSRYTEVKKEDIDKVPELEILAESDEAGVYVVANKSERQIFVTGHPEYDR 239

Qy 241 QTLAQEFFRDVEAGLDPDVPYNYFPHNDPQNTPRASWRSHGNLLFTNWLNYYVYQISYIH 300

Db 240 YTLRDEYYRDIGRNLKVPIPANYFPNDDPTKTPILTWWSHAHLFFSNWLNYCIYQ----- 294

Qy 301 HYLLVNNSTELWMHTRLIKRPH 322

Db 295 ----------KTPY 298

RESULT 9
C97125
homoserine trans-succinylase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97125
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97125
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <KUR>
A;Cross-references: UNIPROT:Q97I29; UNIPARC:UPI000012EF53; GB:AE001437; PIDN:AAK79790.1
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1825
C;Superfamily: homoserine O-succinyltransferase

Query Match 44.5%; Score 790; DB 2; Length 301;
Best Local Similarity 49.8%; Pred. No. 3.2e-26;
Matches 147; Conservative 49; Mismatches 99; Indels 0; Gaps 0;

Qy 1 MPIRVPDELPAVNFLREENVFVMTTSRASGQEIRPLKVLILNLMPKKIETENQFLRLLSN 60

Db 1 MPIKIPDNLPAAKTLNEENIFFMDEDRAYHQDIRPLNIVIVNLMPTKIVTETQILRLIGN 60

Qy 61 SPLQVDIQLLRIDSRESRNTPAEHLNNFYCNFEDIQDQNFDGLIVTGAPLGLVEFNDVAY 120

Db 61 SPLQVNPTFIHTQTHKSQNTSKEHLIKFYETFEEIKNNKFDGMIVTGAPVETLSFENVDY 120

Qy 121 WPQIKQVLEWSKDHVTSTLFVCWAVQAALNILYGIPKQTRTEKLSGVYEHHILHPHALLT 180

Db 121 WEELCRIFDWSVIDVTSTIHICWGAQAGLYHHYGIPKYELHEKLFGVFKHNLTERNIKLT 180

Qy 181 RGFDDSFLAPHSRYADFPAALIRDYTDLEILAETEEGDAYLFASKDKRIAFVTGHPEYDA 240

Db 181 RGFDDEFYAPHSRHTYVKREDIKKNPSLKILAESDEAGAYIVASENGKNIFVMGHAEYDG 240

Qy 241 QTLAQEFFRDVEAGLDPDVPYNYFPHNDPQNTPRASWRSHGNLLFTNWLNYYVYQ 295

Db 241 DTLNLEYIRDKNQGMNIKIPKNYFKDNDPEKGPMVTWRGHANLLFSNWLNYYVYQ 295

RESULT 10
A98051
homoserine O-succinyltransferase (EC 2.3.1.46) [imported] - Streptococcus pneumoniae (s
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 07-Jul-2003
C;Accession: A98051
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: A98051
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <KUR>
A;Cross-references: UNIPARC:UPI00000E365A; GB:AE007317; PIDN:AAL00238.1; PID:g15459089;
C;Genetics:
A;Gene: metA
C;Superfamily: homoserine O-succinyltransferase
C;Keywords: acyltransferase; coenzyme A

Query Match 43.5%; Score 772; DB 2; Length 314;
Best Local Similarity 48.8%; Pred. No. 2.2e-25;
Matches 144; Conservative 53; Mismatches 98; Indels 0; Gaps 0;

Qy 1 MPIRVPDELPAVNFLREENVFVMTTSRASGQEIRPLKVLILNLMPKKIETENQFLRLLSN 60

Db 1 MPIRIDKKLPAVEILRTENIFVMDDQRAAHQDIRPLKILILNLMPQKMVTETQLLRHLAN 60

Qy 61 SPLQVDIQLLRIDSRESRNTPAEHLNNFYCNFEDIQDQNFDGLIVTGAPLGLVEFNDVAY 120

Db 61 TPLQLDIDFLYMESHRSKTTRSEHMETFYKTFPEVKDEYFDGMIITGAPVEHLPFEEVDY 120

Qy 121 WPQIKQVLEWSKDHVTSTLFVCWAVQAALNILYGIPKQTRTEKLSGVYEHHILHPHALLT 180

```
Qy        181 RGFDDSFLAPHSRYADFPAALIRDYTDLEILAETEEGDAYLFASKDKRIAFVTGHPEYDA 240
              |||| |  | ||: :   | |  : :|||| |::|     |    |      ::  | |||:
Db        181 NGFSDDFQVPVSRWTEVRRADIEKHPELEILMESDEMGVCLAHEKAGNRLYMFNHVEYDS 240

Qy        241 QTLAQEFFRDVEAGLDPDVPYNYFPHNDPQNTPRASWRSHGNLLFTNWLNYYVYQ 295
              :|| |:|||| :|:   :|:|||||||:  |   |||| :| | ||:|  :||
Db        241 TSLADEYFRDVNSGVPIKLPHDYFPHNDPELAPLNRWRSHAHLFFGNWIN-EIYQ 294


RESULT 14
C97685
homoserine O-succinyltransferase (homoserine o-transsuccinylase) (hts) [imported] - Agrc
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 07-Jul-2003
C;Accession: C97685
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C97685
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-316 <KUR>
A;Cross-references: UNIPARC:UPI00000D1FCF; GB:AE007869; PIDN:AAK88436.1; PID:g15157931;
C;Genetics:
A;Gene: AGR_C_4927
A;Map position: circular chromosome
C;Superfamily: homoserine O-succinyltransferase

  Query Match           40.1%;  Score 710.9;  DB 2;  Length 316;
  Best Local Similarity  45.4%;  Pred. No. 9.4e-23;
  Matches  134;  Conservative   57;  Mismatches  103;  Indels    1;  Gaps    1;

Qy          1 MPIRVPDELPAVNFLREENVFVMTTSRASGQEIRPLKVLILNLMPKKIETENQFLRLLSN 60
              |||::||  |||    |  | | ||| : |  |:||||:: :||||| ||:|| |  ||:
Db          9 MPIKIPDTLPAFETLVHEGVRVMTETAAIRQDIRPLQIGLLNLMPNKIKTEIQMARLVGA 68

Qy         61 SPLQVDIQLLRIDSRESRNTPAEHLNNFYCNFEDIQDQNFDGLIVTGAPLGLVEFNDVAY 120
              |||||:: |:||    ::||| ||| :||  :|::: : ||| |:||||: |::: || |
Db         69 SPLQVELSLIRIGGHRAKNTPEEHLLSFYQTWEEVRHRKFDGFIITGAPIELLDYEDVTY 128

Qy        121 WPQIKQVLEWSKDHVTSTLFVCWAVQAALNILYGIPKQTRTEKLSGVYEHHILHPHALLT 180
              | :::|: ||:: :| ||| |||   ||:   :|:||    || |||  |  | | ::
Db        129 WNEMQQIFEWTQTNVHSTLNVCWGAMAAIYHFHGVPKYELKEKAFGVYRHRNLSPSSIYL 188

Qy        181 RGFDDSFLAPHSRYADFPAALIRDYTDLEILAETEEGDAYLFASKDKRIAFVTGHPEYDA 240
              || | |  | ||: :   | |  : :|||| |::|     |    |      ::  | |||:
Db        189 NGFSDDFQVPVSRWTEVRRADIEKHPELEILMESDEMGVCLAHEKAGNRLYMFNHVEYDS 248

Qy        241 QTLAQEFFRDVEAGLDPDVPYNYFPHNDPQNTPRASWRSHGNLLFTNWLNYYVYQ 295
              :|| |:|||| :|:   :|::|||||||:  |   |||| :| | ||:|  :||
Db        249 TSLADEYFRDVNSGVPIKLPHDYFPHNDPELAPLNRWRSHAHLFFGNWIN-EIYQ 302


RESULT 15
AD3607
homoserine o-succinyltransferase (EC 2.3.1.46) [imported] - Brucella melitensis (strain
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 07-Jul-2003
C;Accession: AD3607
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AD3607
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-322 <KUR>
A;Cross-references: UNIPARC:UPI00000585FA; GB:AE008918; PIDN:AAL54023.1; PID:g17984975;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0781
A;Map position: II
C;Superfamily: homoserine O-succinyltransferase
C;Keywords: acyltransferase; coenzyme A

  Query Match           36.5%;  Score 647.1;  DB 2;  Length 322;
  Best Local Similarity  38.8%;  Pred. No. 5.6e-20;
  Matches  124;  Conservative   61;  Mismatches  106;  Indels   29;  Gaps    3;

Qy          1 MPIRVPDELPAVNFLREENVFVMTTSRASGQEIRPLKVLILNLMPKKIETENQFLRLLSN 60
              |||::||:||| : |  | | ||  : |  |:||||:: :||||| |: || |  |||
Db         17 MPIKIPDDLPATSVLEAEGVMVMREADAVRQDIRPLRIGLLNLMPNKVTTETQIARLLGA 76

Qy         61 SPLQVDIQLLRIDSRESRNTPAEHLNNFYCNFEDIQDQNFDGLIVTGAPLGLVEFNDVAY 120
              :||||:: |:|: :  :|:|||:|: :||| :|:: || ||| ::||||:  : | :| |
Db         77 TPLQVELTLVRMTNHVARHTPADHMLSFYCPWEEVNDQRFDGFVITGAPVERLPFEEVTY 136

Qy        121 WPQIKQVLEWSKDHVTSTLFVCWAVQAALNILYGIPKQTRTEKLSGVYEHHILHPHALLT 180
              | ::::| :|:: ||  || :||| |||:   :|: |     | |||:    |   :
Db        137 WDEMRRVFDWTQSHVHRTLNICWAAQAAVYHFHGMKKYDLPAKASGVFRQRSLVLASPYL 196

Qy        181 RGFDDSFLAPHSRY-----ADFPAALIRDYTDLEILAETEEGDAYLFASKDKRIAFVTGH 235
              ||| | |  | ||:     :| ||      : |::| :: |    |       |   : |
Db        197 RGFSDDFAIPVSRWTEVRKSDIPAD-----SGLKVLVDSTETGLCLLDDPRHRSLHMFNH 251

Qy        236 PEYDAQTLAQEFFRDVEAGLDPDVPYNYFPHNDPQNTPRASWRSHGNLLFTNWLNYYVYQ 295
              |||  :|| |:|||::   :  || |||| :| :  |   |||| :||| ||:|
Db        252 VEYDTTSLADEYFRDIQVQPEAKVPVNYFPGDDAKRPPENRWRSHAHLLFGNWIN----- 306

Qy        296 ISYIHHYLLVNNSTELWMHT 315
                          |::  |
Db        307 --------------EMYQST 312


Search completed: August  1, 2006, 04:30:16
Job time : 22.8385 secs
```